

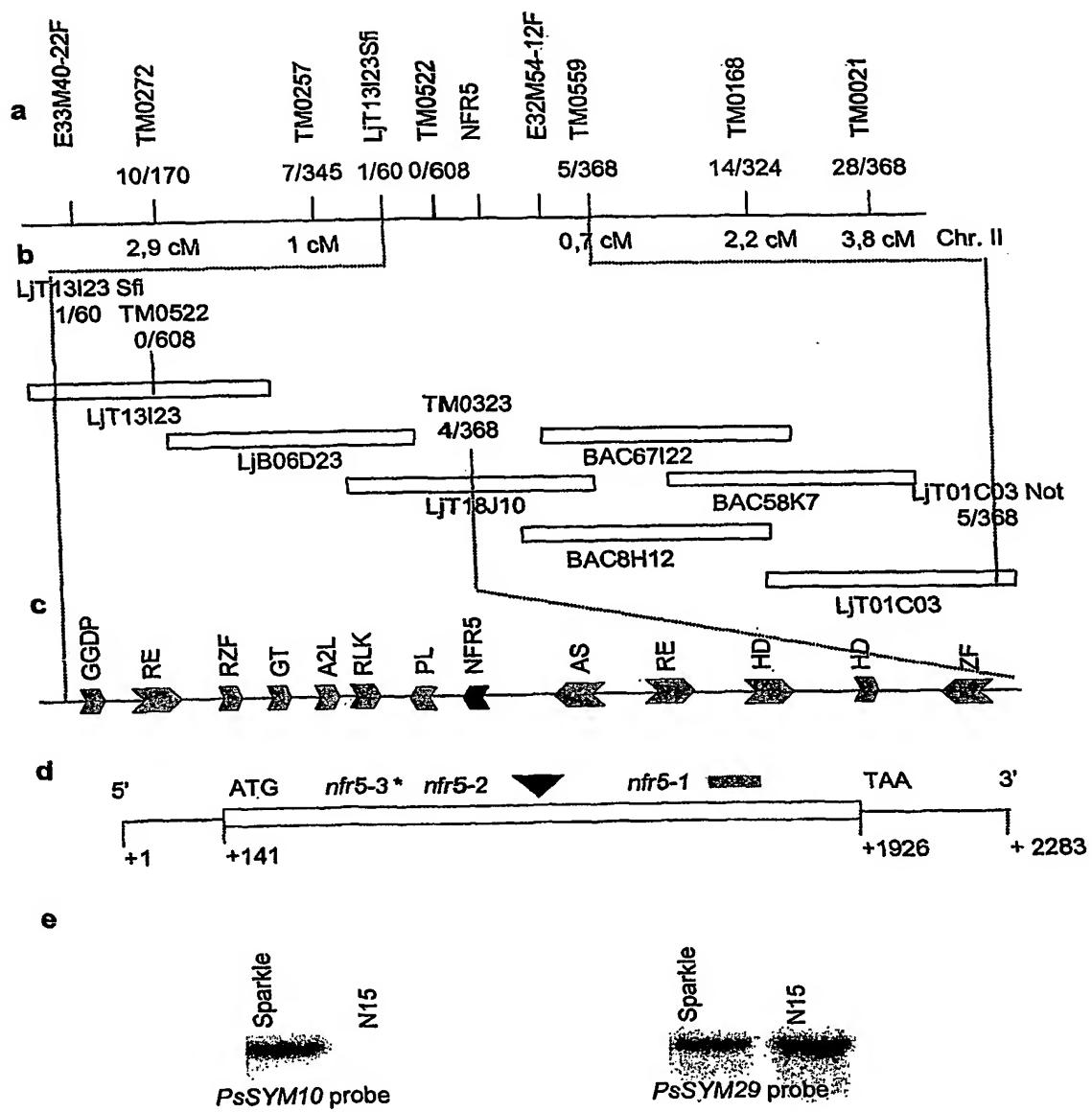
Figure 1

Figure 2**a****b**

MAVFFLTSGSLSLFLALTLLFTNIAA	SP
RSEKISGPDFSCPVDSPPPSCETYVT	51 aa
* YTAQSPNLLSLTNISDIFDISPLSIARASNIDAGKDKLVPQGVLLVP	LysM1
VTCGCAGNHSSANTS	113 aa
YQIQLGDSYDFVATTLYENLTNWNIVQASNPGVNPYLLPERVKVVFP	LysM2
LFCRCPSKNQLNKGIQYLIT	180 aa
YVWKPNNDNVSLVSAKFGASPADILTENRYGQDFTAATNLPIIIP	LysM3
VTQLPELTQPSSNGRKSSIHLL	246 aa
VILGITLGCTLTAVLTGTLVYVYC	TM
RRKKALNRTASSAETADKLL <u>SGVSGYVSKPNVYEIDEI</u>	KD
MEATKDFSDECKVGESVYKANIEGRVVA <u>VAKKIKEGGANEELKILQKV</u>	
NHGNLVKLMGVSSGYDGNCFLVYE <u>YAENGSLAEWLFSKSSGTPNSLT</u>	
WSQRISIAVDVAVGLOQMHEHTYPRI <u>HRDITTSNILLDSNFKAKIA</u>	
NEFAMARTSTNPMPKID <u>VFAFGVLLIELLTGRKAMTTKENGEVVMLW</u>	
KDMWEIFDIEENREERIRKMDPNLESFYHIDNALSLASLAVNCTAD	
KSLS <u>RPSMAEIVLSLSFLTQQSSNPTLERSLTSSGLDVEDDAHIVTS</u>	
ITAR	595 aa

Diagram showing the domain organization of a protein. It consists of a black bar with a hatched pattern on the left, followed by a white bar with black boxes labeled 'SP', 'LysM1', 'LysM2', 'LysM3', 'TM', and 'Kinase' from left to right. The sequence is divided into several domains: SP (51 aa), LysM1 (113 aa), LysM2 (180 aa), LysM3 (246 aa), TM (595 aa), and Kinase. The TM domain is further divided into 11 sub-domains labeled I through XI. The sub-domains are: I (MEATKDFSDECKVGESVYKANIEGRVVAVAKKIKEGGANEELKILQKV), II (NHGNLVKLMGVSSGYDGNCFLVYEYAENGSLAEWLFSKSSGTPNSLT), III (WSQRISIAVDVAVGLOQMHEHTYPRIHRDITTSNILLDSNFKAKIA), IV (NEFAMARTSTNPMPKIDVFAFGVLLIELLTGRKAMTTKENGEVVMLW), V (KDMWEIFDIEENREERIRKMDPNLESFYHIDNALSLASLAVNCTAD), VIa (KSLSRPSMAEIVLSLSFLTQQSSNPTLERSLTSSGLDVEDDAHIVTS), VII (ITAR), VIII (Kinase), IX (TM), X (TM), XI (TM).

Figure 2**c**

NFR5M1	52 : YTAOSPNLLSLTNISDIFDISPLSIARASNEDAGKDKLVEGOVLLVP : 98
SYM10M1	52 : YFARSPNFLSLTNISDIFDMSPLSIAKASNTEDEPKKLVEGOVLLIP : 98
M.tM1	53 : YRAOSPNLTLISLSNISDIFNLSPLRIAKASNTEAEDKKLIEDQLLLVP : 99
RiceM1	47 : YRTOSPCFLDLGNISDLFGVSRALIASANKLTTEGVLLVEGOPLLVP : 93
NFR5M2	114 : YQIQLGDSYDFVATLILEYENIENWNNIQASNPGVNPYILPERVIVWFP : 160
SYM10M2	114 : YIIEKLGDNYEVLSITSYQNLINYVEMENFNPNESPNILLEPEIKVAMP : 160
M.tM2	115 : YSIKQGDNEFLSITSYQNLINYLEFKNFNPNSPILPLDTEKSVVP : 161
RiceM2	109 : YPIIRPRDTEEGLAVIAFENIIDFVILVEELNEAAEATRLEPWOEAVVP : 155
VolvoxM2	106 : YIHQPGDIEWAIAQR.RG...ITVDVIQSENEPGVNPARIQVGOVINVP : 149
Pfam	1 : YTVIKKGDTLWKIARR. V.G..ISVSELKSLN.GESSDNLVYCGOKLKIP : 43
NFR5M3	181 : YVWKENDNVSVLSVSAKIGASPAIITENRYGDTTAATNLIEILIP : 224
SYM10M3	181 : YVWCANDNVTRVSSKGEGASGVDMFTEN...NONETASTNVEILIP : 222
M.tM3	182 : YVWCIDNDNVTVVSKEKGASGVEMGAEN...NNNETASTMRSVLIP : 223
RiceM3	176 : YVWQPGDDVSVVSALMNASAANIAASNGVAGNSTFATGQEVLIB : 219

d

	VII	VIII	IX
Cons	...DFG.....	...APE.....	...D.W..G
Smart	195 : KIADEGLS...DLYSDYYKVKGGKLPIRWMADPSLKEGKFTSKSDVWSFG : 248		
Arab	500 : KIANFGVARILDEGDLQLTRHVEGTQGYLAREYVENGVITSKLDVFAFG : 550		
NFR5	448 : KIANFAMARSH... : 448	PMMPGIDVFAFG : 472	
SYM10	449 : KIANFSMARTSH... : 449	SMMPKIDVFAFG : 473	
M.t	450 : KIANFGMARSH... : 450	SMMPKIDVFAFG : 474	
Rice	476 : KLSNESLAKPAAMV... : 476	AAATSSDVEAFG : 502	

Figure 3

Lotus 1: MVEELTGSISLFLLT. LLENTIAARSEKIS. PDFSCPVDSPPSETTYVYTAWSPNLLSCLNENSDIF. ISPLIITARA: 79
 Pea 1: MIEFLSESSEFLFLA. VNTIAAEQ. QIS. PDFSCPVDSPPSETTYVYFARSPPNLLSCLNENSDIF. ISPLIITARA: 79
 M.t 1: MSAFFLSSSFLFLVLL. KNTIA. YSET. PDFSCPVDSPPSETTYVAYRA. SPPNLLSCLNENSDIF. ISPLIITARA: 80

Lotus 80: SNIDGKDKL. QLLN PVTCCAGNE. SANTSIOIONGDS. DFLATLYENLTNNTVOASNPGVNWLPERVKVLF: 159
 Pea 80: SNIDGKDKL. QLLN PVTCCAGNE. SANTSIOIONGDS. DFLATLYENLTNNTVOASNPGVNWLPERVKVLF: 159
 M.t 81: SNIDGKDKL. DOLLN PVTCCAGNE. SANTSIOIONGDS. DFLATLYENLTNNTVOASNPGVNWLPERVKVLF: 160

Lotus 160: PLEFCESKNQNLKGIONLITYWKKENDNVS. VSAKEGASPA. I. ENYGC. DFLTAATNL. LLIPTVQLE. TQSSNGR: 239
 Pea 160: PLEFCESKNQNLKGIONLITYWKKENDNVS. VSAKEGASPA. I. ENYGC. DFLTAATNL. LLIPTVQLE. TQSSNGR: 237
 M.t 161: PLEFCESKNQNLKGIONLITYWKKENDNVS. VSAKEGASPA. I. ENYGC. DFLTAATNL. LLIPTVQLE. TQSSNGR: 238.

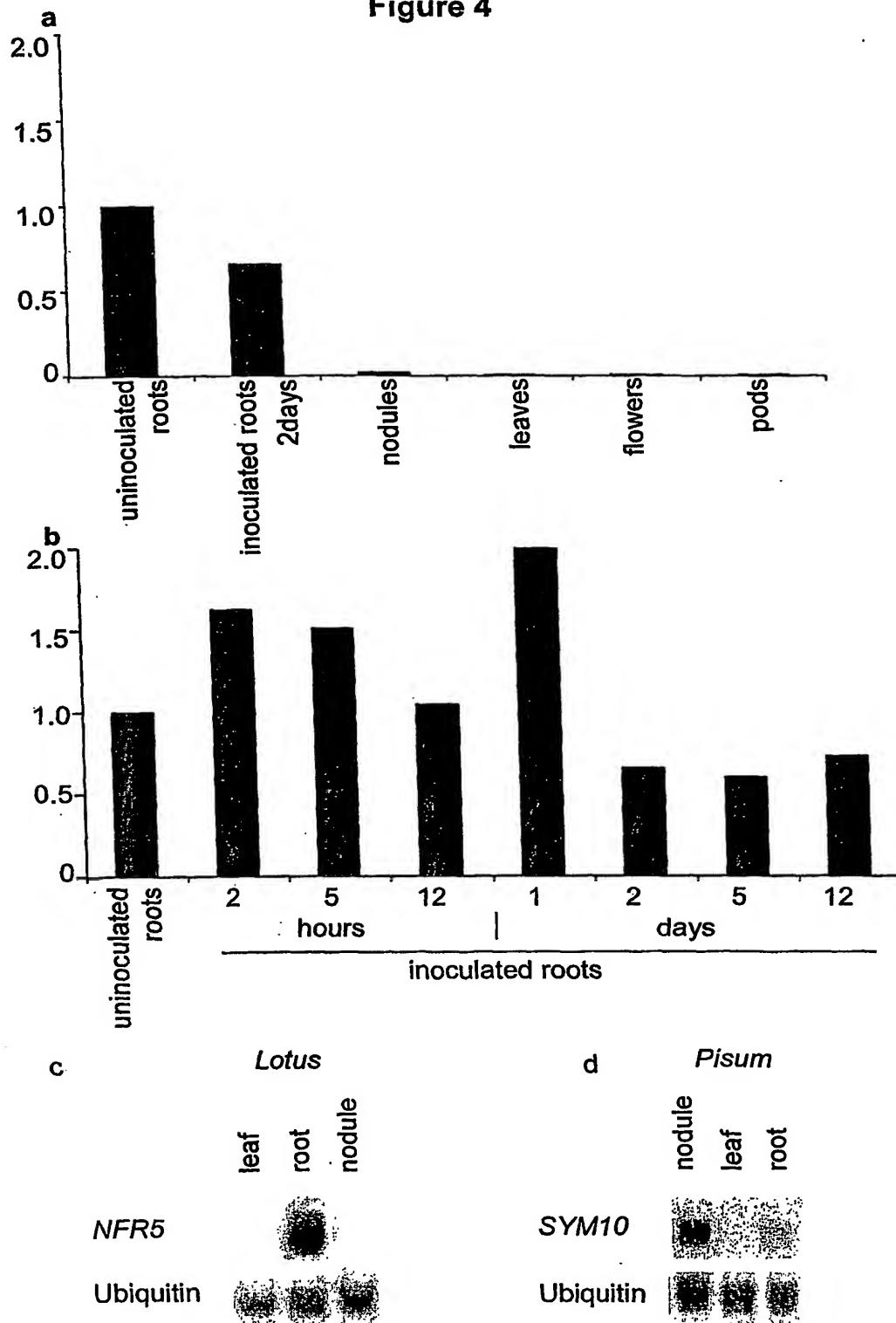
Lotus 240: K. S. IIR. LVLIGLIG. LLLTAVLT. GLVVYVYCRKKALNRTA. SETADKLL. LSGVSGVSKP. VEN. D. I. M. E. T. M. SE: 318
 Pea 238: K. S. IIR. LVLIGLIG. LLLTAVLT. GLVVYVYCRKKALNRTA. SETADKLL. LSGVSGVSKP. VEN. D. I. M. E. T. M. SE: 317
 M.t 239: K. S. IIR. LVLIGLIG. LLLTAVLT. GLVVYVYCRKKALNRTA. SETADKLL. LSGVSGVSKP. VEN. D. I. M. E. T. M. SE: 318

Lotus 319: ECKUGESVYKANIEGRVVAVKKKIEGGANBEKKL. LOKVNHGNL. VKL. MGSSGY. GNCFLVVEYAENGSL. AEMLFS. SGT: 398
 Pea 318: ECKUGESVYKANIEGRVVAVKKKIEGGANBEKKL. LOKVNHGNL. VKL. MGSSGY. GNCFLVVEYAENGSL. AEMLFS. SGT: 396
 M.t 319: ECKUGESVYKANIEGRVVAVKKKIEGGANBEKKL. LOKVNHGNL. VKL. MGSSGY. GNCFLVVEYAENGSL. AEMLFS. SGT: 397

Lotus 399: PN. SITWSQRI. ANDVA. GLQYMEHTYPRITHDITTSNLL. SINFKAKIANFAMARTSTN. MMPKCDVFAFGVLL: 475
 Pea 397: PN. SITWSQRI. ANDVA. GLQYMEHTYPRITHDITTSNLL. SINFKAKIANFAMARTSTN. MMPKCDVFAFGVLL: 476
 M.t 398: PN. SITWSQRI. ANDVA. GLQYMEHTYPRITHDITTSNLL. SINFKAKIANFAMARTSTN. MMPKCDVFAFGVLL: 477

Lotus 476: IELLTGKA. T. T. ENGEVVL. KWD. I. T. ENREE. IRKWMDDENLE. FY. T. D. N. A. L. S. L. A. V. N. C. T. A. D. K. S. L. S. R. P. MAEI: 555
 Pea 477: IELLTGKA. T. T. ENGEVVL. KWD. I. T. ENREE. IRKWMDDENLE. FY. T. D. N. A. L. S. L. A. V. N. C. T. A. D. K. S. L. S. R. P. AEI: 556
 M.t 478: IELLTGKA. T. T. ENGEVVL. KWD. I. T. ENREE. IRKWMDDENLE. FY. T. D. N. A. L. S. L. A. V. N. C. T. A. D. K. S. L. S. R. P. AEI: 557

Lotus 556: VI. SISFL. TQOSSNPLERSLTSGL. EDDAE. IVTS. TAR: 595
 Pea 557: VI. SISFL. TQOSSNPLERSLTSGL. EDDAE. IVTS. VAR: 594
 M.t 558: VI. SISFL. TQOSSNPLERSLTSGL. EDDAE. IVTS. VAR: 595

Figure 4

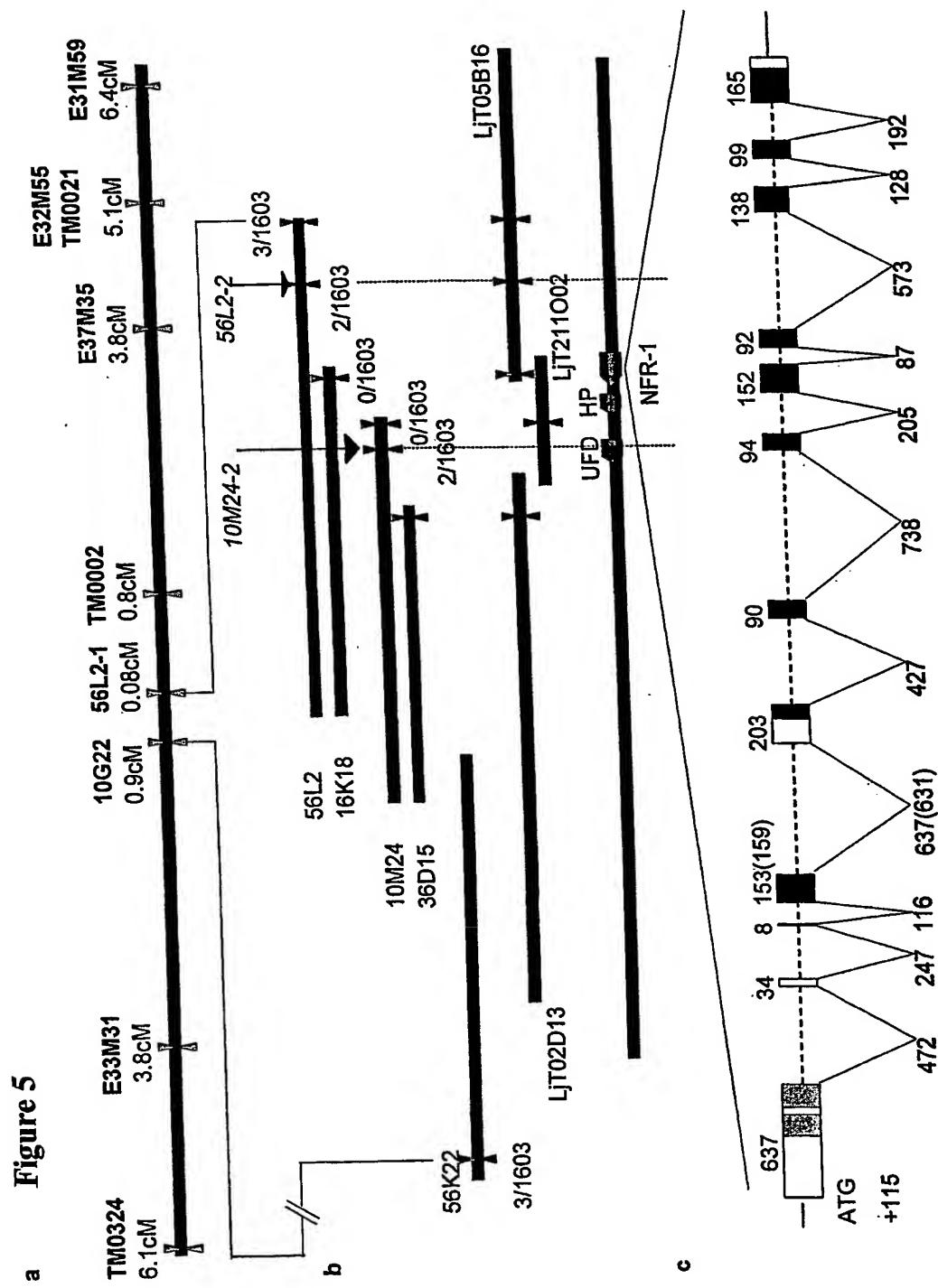


Figure 6

a

MKLKTGLLLFFILLLGH	SP
VCFHVESNCLKGCDLALASYYILPGVFIQNITTFMQSEIVSSNDAITS YNKDKILNDINIQSQRNLIPFFCPCDCIGGEFLGHVFE	103
<u>YSASKGDTYETIANLYYANLTTVDLLKRFNSYDPKNIPVNAKVNT</u>	LysM1
VNCSCGNSQVSQSKDYGLFIT	168
<u>YPIRPGDTLQDIANQSSL DAGLIQSFnPSVNF SKD SGIAFIP</u>	LysM2
GRYKNGVYVPLYHR	224
TAGLASGAAVGISIAGTFVLLLAFCMYV	TM
RYQKKEEEKAKLPTDISMALSTQD (GN)A SSSAEYETSGSSGPGTASAT GLTSIMVAKSMEFSYQELAKATNN	322 (324)
FSLDNKIG <u>QGGFGAVVY</u> AELRGKKTA <u>IKKMDVQ</u> ASTE <u>FLCEL</u> KVLTHV I II III	KD
<u>HHNLNLVRLIGY</u> CVEGSLFLVYEH <u>IDNGNLGQYLHGSGKEPL</u> PWSSRVOIA IV V VIa	
<u>LDAARGLEYI</u> HEHTVPVYI <u>HRDVKSANILID</u> KNLRGKVA <u>DGLTKLIEVG</u> VIa VII	
NSTLQTRLV <u>GTFGYMPPEY</u> AQYGDISPKID <u>VYAFGVVL</u> FELISAKNAVLT VIII * IX	621 (623)
GELVAESKGLVALFEEALNKSDPCDALRKLVDPRLGENYPIDSVLKIAQLG *	
RACTRDNP <u>LLRPSMRS</u> LVVALMTLSSLTEDCDDESSYESQLINLLSVR*	
XI	

b

SMART0257	YTVKKEDTILSSIIARRGIVSVS--DIELNNIIPDNLOGOAKIP-
NFR1-M1	104 YSASKGDTYETIANLYYANLTTVDLLKRFNSYDPKNIPVNAKVNT-- 149
At21630-M1	105 YSASKGDTYETIANLYYANLTTVDLLKRFNSYDPKNIPVNAKVNT-- 151
SMART0257	YTVKKEDTILSSIIARRGIVSVS--DIELNNIIPDNLOGOAKIP-
NFR1-M2	167 YPIRPGDTLQDIANQSSL DAGLIQSFnPSVNF SKD SGIAFIP- 208
At21630-M2	170 YPLREEDSISSIIARRGIVSVS--DIELNNIIPDNLOGOAKIP- 211
BAB89226-M2	168 MAVQDGDVGNITASLFRSWKDELDNERVANPDFIKPFWLFP- 212
Volvox M	42 YTIQEGDIFWAIQORRGTTVDVLSN--GIVFARLQVQVINVP- 85

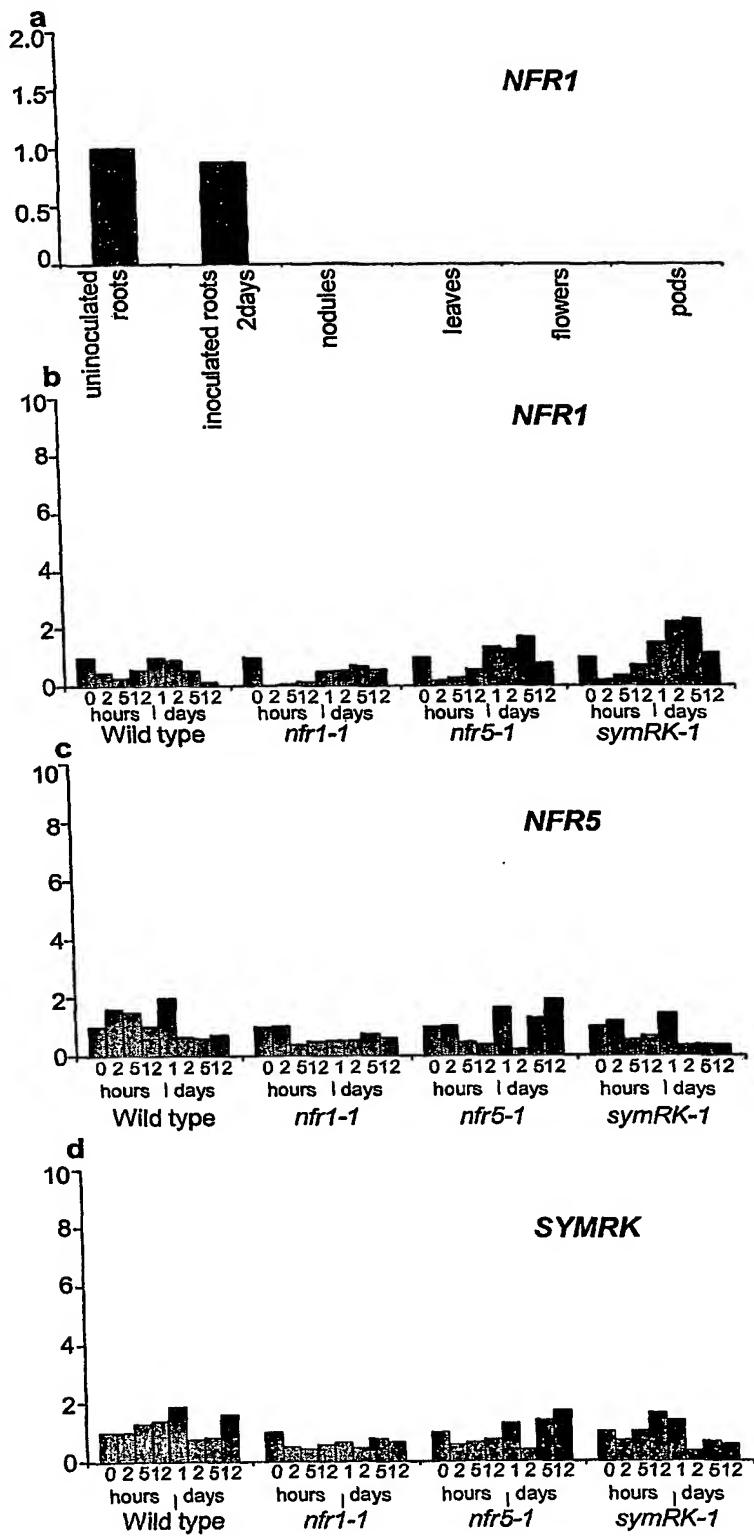
Figure 7

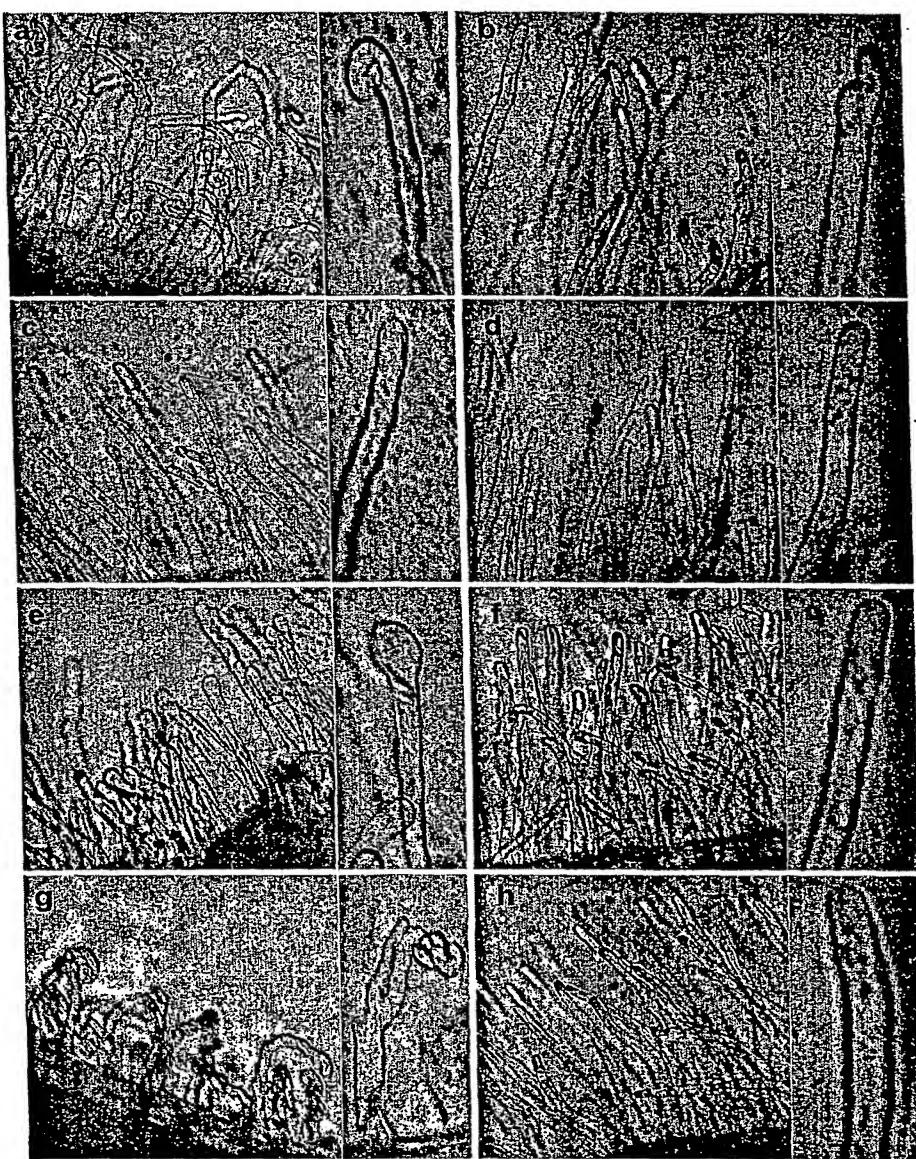
Figure 8

Figure 9

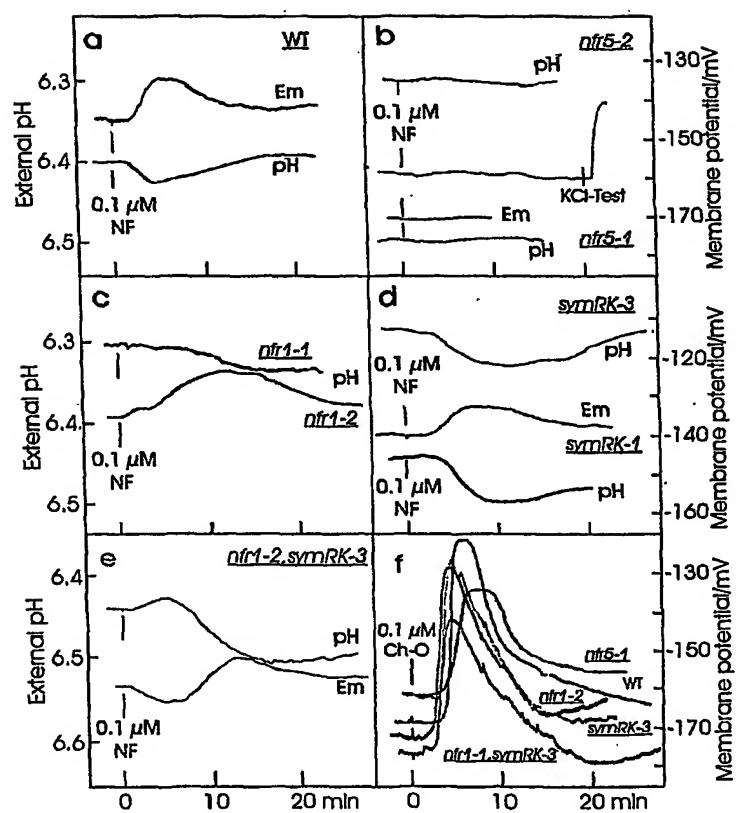


Figure 10

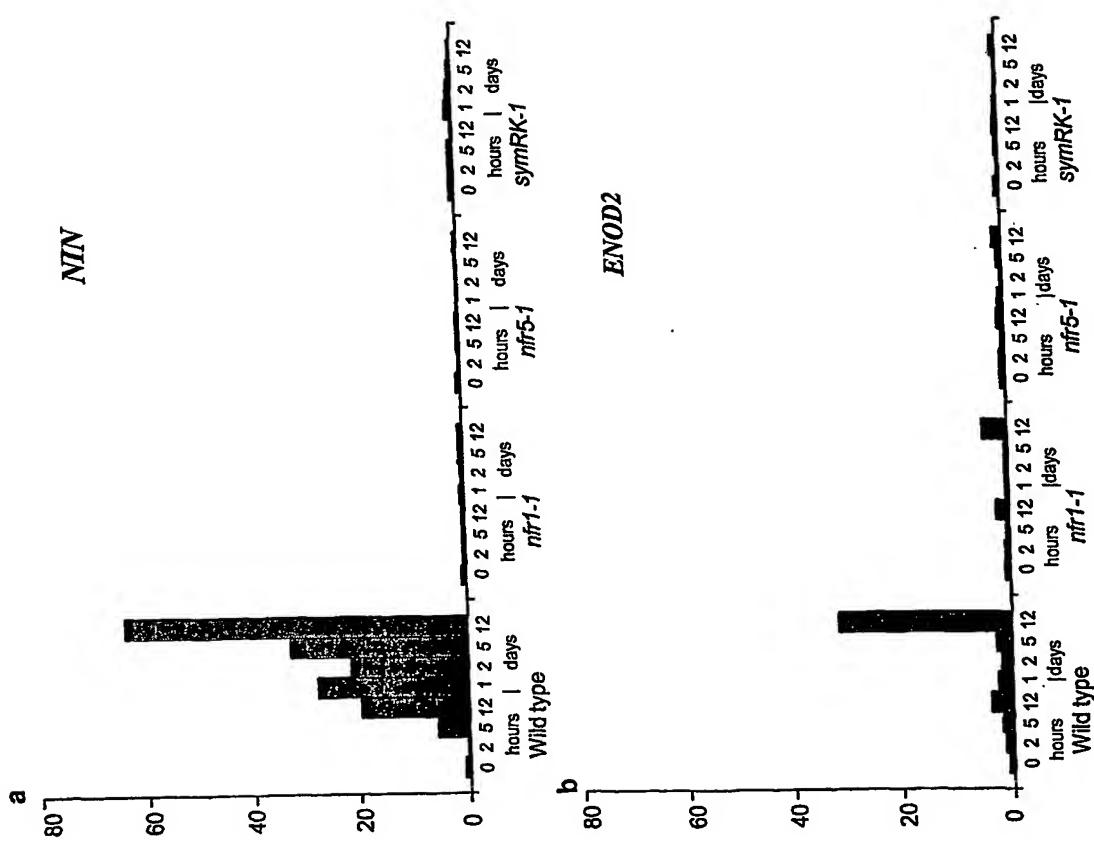


Figure 11

NFR1 1: MK... LKIG. LILFIL LIGHTCFHVE SINCLKG... C. D. LALASVIL... FGFIJIONITITM QSEITVSSNDAITSYNKKDKILNDINIOSFORI
NFR5 1: MAVFFLTSGLSISLTLA TLLFTNIAARSEKISGPDFSCPVDSPESETVTAQSPNLLISLTNISDIFDISPLSIARAS... NIDAGK. DKLVPG. QVL

NFR1 85: NIEFFPCDCICGEFLGHVFEYSASKGDIYETIANLYANLTVDLILKREN. SYDEFKNIPVNAKVNNTVNCSCGNS. QVSKRDYGLFITYPIRPGDTILODIAN
NFR5 96: LVEVTCGAGAHHSSANT. SKIQLQGDSYDFVATLTYENLTNNWNTVQASNPGVNPYLLPERVKKVTPFLFCRCPSKNQLNKGQIQLITYVWVKPNDNVSLVSA

NFR1 183: OSSLDAGLHOSTEN. PSVNFESKDSGI. AFI PGRYKNGVVFPLYHRTAGLASSAAGVISTAGTFVILLAFCMYVRYQKKEEKAKLPTDISMALSTQDASS
NFR5 195: KFGASPADTILTENRYQDFTAATNLPLIP... VT. QLPETIOPS. SNGRKS. SIELLIVT. GLITLGCTIL. TAVLTGTLVVYCREKKALN. RTASS

NFR1 281: SAEYETSGSSCPGTASATGLLISIMVAKSMEFSYQELAKATNNFSLDNKIGQGGFCAVYAEFLRKKTAALKMDVQASTEFLCELKVLTTHHLINVRIG
NFR5 283: AETADKLLSG... VSGY... VSKPNVEIDEIMEATKODESDECKVGES... VYKANIEGRVAVAKKKIKEGGANE... ELKILQYVNHGNLVKLMG

NFR1 381: YC. VEGSLELVYEHIDNGNIGOYHNG. SGKEF. LPWSSRVQIAIDAAARGLEYIHTHTVPIIHRDVKSANTIDKNULRGRVADEGLITKLIEVGNSTLQ
NFR5 367: VSSGYIGNCFLVYEAENGSLAEMLFSSKGSGTPNSLTIWSORISIAVDAVGLQYMHEHTYPRIIHRDITTSNLLDSTFKAJIANFAMAR... TST...

NFR1 476: TRLVGTIEGYMPEPEYAQYGDISPKIDVYAFGVVLEELISAKNAVL.. KIGELVVAESKGGLYVALFEELANKSDPCDAIRKLIVDPRIGENYPTDSVVKIAOLGR
NFR5 459: ... NP... MNPKLIDVFAFGVILLIELITGRKAMTTKENGEVMLWKDMWEIFDIEENR... EERIRKWMDDPNLESFYHDDNALISLAV

NFR1 574: ACTRDNPILURPSMRSIVVALMNTSSLTEDCDESSYES... QTLINLLSVR
NFR5 540: NCTADKSLSRPSMAEIVLISLISFLTOQSSNPTLERSINTSGLDVDDAHIVTSITAR

Figure 12
Protein domain structure of *Lotus japonicus* and *Lotus filicaulis* NFR1 and NFR5 proteins and of the hybrid proteins

